

```
SEQUENCE LISTING
<110> FULTON, CHANDLER
      LAI, ELAINE Y.
<120> THIAMINASES AND THIAMINASE GENES FOR USE IN APOPTOTIC
      THERAPIES
<130> 073442-0301
<140> 09/675,509
<141> 2000-09-29
<150> 60/052,377
<151> 1997-07-11
<150> 60/087,526
<151> 1998-06-01
<150> 60/156,952
<151> 1999-09-29
<160> 23
<170> PatentIn Ver. 2.1
<210> 1
<211> 3078
<212> DNA
<213> Naegleria gruberi
atgtccactc aaccaaagac actcactgtt ggtctcttcc catatcttcc ttcttggaat 60
gaaaatggca acgaagttaa attgatcaat ttgatcaagg atgttttgcc aactcaggtt 120
tccggatata atatcgaata taccgaattt gattgttaca gtgatgctag tcttcaaagt 180
cttccagatg ttttctcaac tgatagcatt ttccttccat atcttgtttc tttgggtggt 240
gtcaagagtt tggatgaatc attggttcgt ggtgttactg gtgatttgca tagttttgtt 300
tecteaagtg cetetgteaa tggtteegtt tatggtttee cacaataett gtgeteaaac 360
tttttattgt cctcaccaaa tggtactcaa caagcatctt cccttttaga attggctcaa 420
aaggttggtt atgaacaaat tgtttatcca gatgttgcct cttctagttc tttcacagtt 480
ttcggattgt atcaacaatt actccaatca tcatcatcag ctgcagttga tatcaaggcc 540
tctgatcttc cacaatctgg tgaccaagtc aacaaggata tcactcaaaa atatagaacc 600
attttggatt caacagttgt tgcctctcaa agagaatata ttaactctgt aaagcaaggt 660
aaaccaattt caaactacta tgtcggatat agtgaaagta tgtgtgaaat taaggatatc 720
atcagagatc aacaatacaa tgttcaactc attggtacct ctgataagcc atacgtttat 780
actgatgttt tggctttgaa ttccaatttg tgtgatgaaa agcaaaaggt tgctgttgaa 840
gttatcaaga atttattgac taatacttta gttttggact tgttgggtct cggattaact 900
ctcccagcca acaagaatgg tattgctcat ttggctaaat catcaaactt ttatgctcaa 960
ttgagccaac aattcgatgc caaggaaagt gaagttagag ttttgagatg tgttgacttt 1020
gctaacaagg aagttaagaa ttgtgctggt gtcttgagac cattccttca acatattgct 1080
gttgctactt tgcgttgttt gactgctgac actgtcgaaa aggctaagag tggtcaccct 1140
ggtatgccaa ttggtatgtc accaattgcc tatgttttgt ggaagttctt cttcaaatca 1200
tctaaggatg atgtcaattg gttgaacaga gatagatttg ttttgagtaa tggtcacqqt 1260
tgtacattgc tttatgccat gttgcacctc actgattgta acttgagttt ggatgatctc 1320
aagaatttca gaagtttgca ttccaaqact cctgqtcacc caqaatatqq tcacactqaa 1380
ggtgttgatg ctactactgg tccattgggt caaqqtqttt qtaatqctat tqqtatqqct 1440
ctctctgaag ctcacttqqc tqctcqtttc aataaqqatq qacaaaatat ctttqatcac 1500
cacacctatg ttttccttgg tgatggttgt ttgatggaac gtgttgctat ggaaqqtctc 1560
```

```
tcatttgctg gtcaccaaaa gttgaacaag ttgattgttt tctatgatga caatagtatt 1620
actattgatg gtaagactga attgaccttt actcaaaata ctccagaagt catgagaggt 1680
tttggatggc acgtaattgt tgtcgacaag gctgataatg acttggttgg tattaaggaa 1740
gctattttgg aagctcacac tgttactgac aagccaatca tgatcgtttg taagactaca 1800
attggttatt cctcaaaggt tcaaggtact gctaaggttc acggttctcc attgggtgct 1860
gatggattga agaatttgaa ggaaacttgt ggtttcactg gtaatgattt cttccatgtt 1920
ccagaaattg tcagaaagga ctttgctact gtcattaata gaaatagtga aaagctctct 1980
caatggaagc aagttaaatc tgcctatgat accactcatg ctactgaatc ccaactcctc 2040
caaagaatga ttaatcacga attggaaggt gatgttatgg aaaagttgcc aaaatacctc 2100
gaacaaaaga agattgctac cagatctaca tctcaacaag ttttgaatgc catctatcca 2160
ctcattcctt ctctcgttgg tggttcagct gacttgactc catccaactt gactgatgta 2220
actggatgtc aagatttcca accaaacaat agagttggta gatatatcag atttggtgtc 2280
cgtgaacatg ccatggttgc tattgccaat ggtattctct atcatggtgt tcttagaacc 2340
tatgttggta cattcttgaa ctttgcttca tatgctttgg gtgctatcag attgagtgcc 2400
ttgtctggtc ttccaaatat ttatgttttc actcatgaca gtattggtct tggtcaagat 2460
ggtccaactc accaacctgt tgaagtttta ccaatgttga tagccattcc aaatcacatt 2520
gttttcagac ctgctgatgg tagagaaacc agtggtgctt atttgtgggc tgttcaatca 2580
aagaagactc catcctcaat gattctttct cgtcaagatt tgccacaatt gactggtact 2640
gatatttcaa aggttgcttt gggtgcctat gttatccaag gtgatgctac tcctqatqtt 2700
gtccttgttg gtactggttc tgaaqtttcc ctcatqqttq aaqctqctqa aaaqttqaaq 2760
gctaacctta aggttaacgt tgtttccatg ccaagttggg aattgtttgt tcgtcaatca 2820
gaagaataca ggaagactgt cttcccagat ggtattccag ttgtcagtgc cgaagcttca 2880
tcaacctttg gttggacaag ctttgctcac tatgctgttg gtatgactac tttcggtgct 2940
agtgctgctg ctgaagaagt ttacaaactc ctcaagatta cctcagacaa tgttgctgaa 3000
aaggccacca aattggttac caagtatggt aagcaagctc caagactcag cttgtctctt 3060
gttggtgaag aactctaa
                                                                  3078
```

```
<210> 2
```

<211> 1025

<212> PRT

<213> Naegleria gruberi

## <400> 2

Met Ser Thr Gln Pro Lys Thr Leu Thr Val Gly Leu Phe Pro Tyr Leu
1 5 10 15

Pro Ser Trp Asn Glu Asn Gly Asn Glu Val Lys Leu Ile Asn Leu Ile 20 25 30

Lys Asp Val Leu Pro Thr Gln Val Ser Gly Tyr Asn Ile Glu Tyr Thr 35 40 45

Glu Phe Asp Cys Tyr Ser Asp Ala Ser Leu Gln Ser Leu Pro Asp Val 50 55 60

Phe Ser Thr Asp Ser Ile Phe Leu Pro Tyr Leu Val Ser Leu Gly Gly 65 70 75 80

Val Lys Ser Leu Asp Glu Ser Leu Val Arg Gly Val Thr Gly Asp Leu 85 90 95

His Ser Phe Val Ser Ser Ser Ala Ser Val Asn Gly Ser Val Tyr Gly
100 105 110

Phe Pro Gln Tyr Leu Cys Ser Asn Phe Leu Leu Ser Ser Pro Asn Gly 115 120 125

Thr Gln Gln Ala Ser Ser Leu Leu Glu Leu Ala Gln Lys Val Gly Tyr 135 Glu Gln Ile Val Tyr Pro Asp Val Ala Ser Ser Ser Phe Thr Val 155 Phe Gly Leu Tyr Gln Gln Leu Leu Gln Ser Ser Ser Ala Ala Val Asp Ile Lys Ala Ser Asp Leu Pro Gln Ser Gly Asp Gln Val Asn Lys Asp Ile Thr Gln Lys Tyr Arg Thr Ile Leu Asp Ser Thr Val Val Ala Ser Gln Arg Glu Tyr Ile Asn Ser Val Lys Gln Gly Lys Pro Ile Ser Asn Tyr Tyr Val Gly Tyr Ser Glu Ser Met Cys Glu Ile Lys Asp Ile 235 Ile Arg Asp Gln Gln Tyr Asn Val Gln Leu Ile Gly Thr Ser Asp Lys 250 Pro Tyr Val Tyr Thr Asp Val Leu Ala Leu Asn Ser Asn Leu Cys Asp 265 Glu Lys Gln Lys Val Ala Val Glu Val Ile Lys Asn Leu Leu Thr Asn 280 Thr Leu Val Leu Asp Leu Leu Gly Leu Gly Leu Thr Leu Pro Ala Asn Lys Asn Gly Ile Ala His Leu Ala Lys Ser Ser Asn Phe Tyr Ala Gln 305 Leu Ser Gln Gln Phe Asp Ala Lys Glu Ser Glu Val Arg Val Leu Arg Cys Val Asp Phe Ala Asn Lys Glu Val Lys Asn Cys Ala Gly Val Leu Arg Pro Phe Leu Gln His Ile Ala Val Ala Thr Leu Arg Cys Leu Thr Ala Asp Thr Val Glu Lys Ala Lys Ser Gly His Pro Gly Met Pro Ile Gly Met Ser Pro Ile Ala Tyr Val Leu Trp Lys Phe Phe Lys Ser Ser Lys Asp Asp Val Asn Trp Leu Asn Arg Asp Arg Phe Val Leu Ser 410 Asn Gly His Gly Cys Thr Leu Leu Tyr Ala Met Leu His Leu Thr Asp 420 425

Cys Asn Leu Ser Leu Asp Asp Leu Lys Asn Phe Arg Ser Leu His Ser Lys Thr Pro Gly His Pro Glu Tyr Gly His Thr Glu Gly Val Asp Ala Thr Thr Gly Pro Leu Gly Gln Gly Val Cys Asn Ala Ile Gly Met Ala 475 Leu Ser Glu Ala His Leu Ala Ala Arg Phe Asn Lys Asp Gly Gln Asn Ile Phe Asp His His Thr Tyr Val Phe Leu Gly Asp Gly Cys Leu Met 505 Glu Arg Val Ala Met Glu Gly Leu Ser Phe Ala Gly His Gln Lys Leu Asn Lys Leu Ile Val Phe Tyr Asp Asp Asn Ser Ile Thr Ile Asp Gly Lys Thr Glu Leu Thr Phe Thr Gln Asn Thr Pro Glu Val Met Arg Gly 555 545 560 Phe Gly Trp His Val Ile Val Val Asp Lys Ala Asp Asn Asp Leu Val 570 Gly Ile Lys Glu Ala Ile Leu Glu Ala His Thr Val Thr Asp Lys Pro 580 585 Ile Met Ile Val Cys Lys Thr Thr Ile Gly Tyr Ser Ser Lys Val Gln 600 Gly Thr Ala Lys Val His Gly Ser Pro Leu Gly Ala Asp Gly Leu Lys 610 615 Asn Leu Lys Glu Thr Cys Gly Phe Thr Gly Asn Asp Phe Phe His Val 630 Pro Glu Ile Val Arg Lys Asp Phe Ala Thr Val Ile Asn Arg Asn Ser 645 Glu Lys Leu Ser Gln Trp Lys Gln Val Lys Ser Ala Tyr Asp Thr Thr His Ala Thr Glu Ser Gln Leu Leu Gln Arg Met Ile Asn His Glu Leu Glu Gly Asp Val Met Glu Lys Leu Pro Lys Tyr Leu Glu Gln Lys Lys Ile Ala Thr Arg Ser Thr Ser Gln Gln Val Leu Asn Ala Ile Tyr Pro 715 Leu Ile Pro Ser Leu Val Gly Gly Ser Ala Asp Leu Thr Pro Ser Asn

730

Leu Thr Asp Val Thr Gly Cys Gln Asp Phe Gln Pro Asn Asn Arg Val
740 745 750

Gly Arg Tyr Ile Arg Phe Gly Val Arg Glu His Ala Met Val Ala Ile 755 760 765

Ala Asn Gly Ile Leu Tyr His Gly Val Leu Arg Thr Tyr Val Gly Thr 770 775 780

Phe Leu Asn Phe Ala Ser Tyr Ala Leu Gly Ala Ile Arg Leu Ser Ala 785 790 795 800

Leu Ser Gly Leu Pro Asn Ile Tyr Val Phe Thr His Asp Ser Ile Gly 805 810 815

Leu Gly Gln Asp Gly Pro Thr His Gln Pro Val Glu Val Leu Pro Met 820 825 830

Leu Ile Ala Ile Pro Asn His Ile Val Phe Arg Pro Ala Asp Gly Arg 835 840 845

Glu Thr Ser Gly Ala Tyr Leu Trp Ala Val Gln Ser Lys Lys Thr Pro 850 855 860

Ser Ser Met Ile Leu Ser Arg Gln Asp Leu Pro Gln Leu Thr Gly Thr 865 870 875 880

Asp Ile Ser Lys Val Ala Leu Gly Ala Tyr Val Ile Gln Gly Asp Ala 885 890 895

Thr Pro Asp Val Val Leu Val Gly Thr Gly Ser Glu Val Ser Leu Met 900 905 910

Val Glu Ala Ala Glu Lys Leu Lys Ala Asn Leu Lys Val Asn Val Val 915 920 925

Ser Met Pro Ser Trp Glu Leu Phe Val Arg Gln Ser Glu Glu Tyr Arg 930 935 940

Lys Thr Val Phe Pro Asp Gly Ile Pro Val Val Ser Ala Glu Ala Ser 945 950 955 960

Ser Thr Phe Gly Trp Thr Ser Phe Ala His Tyr Ala Val Gly Met Thr 965 970 975

Thr Phe Gly Ala Ser Ala Ala Ala Glu Glu Val Tyr Lys Leu Leu Lys 980 985 990

Ile Thr Ser Asp Asn Val Ala Glu Lys Ala Thr Lys Leu Val Thr Lys 995 1000 1005

Tyr Gly Lys Gln Ala Pro Arg Leu Ser Leu Ser Leu Val Gly Glu Glu 1010 1015 1020

Leu 1025

```
<210> 3
<211> 1068
<212> DNA
<213> Naegleria gruberi
<220>
<221> CDS
<222> (1)..(1068)
<400> 3
atg tcc act caa cca aag aca ctc act gtt ggt ctc ttc cca tat ctt
                                                                   48
Met Ser Thr Gln Pro Lys Thr Leu Thr Val Gly Leu Phe Pro Tyr Leu
cct tct tgg aat gaa aat ggc aac gaa gtt aaa ttg atc aat ttg atc
Pro Ser Trp Asn Glu Asn Gly Asn Glu Val Lys Leu Ile Asn Leu Ile
aag gat gtt ttg cca act cag gtt tcc gga tat aat atc gaa tat acc
Lys Asp Val Leu Pro Thr Gln Val Ser Gly Tyr Asn Ile Glu Tyr Thr
         35
gaa ttt gat tgt tac agt gat gct agt ctt caa agt ctt cca gat gtt
Glu Phe Asp Cys Tyr Ser Asp Ala Ser Leu Gln Ser Leu Pro Asp Val
     50
                         55
tto toa act gat ago att tto ott oca tat ott gtt tot ttg ggt ggt
                                                                   240
Phe Ser Thr Asp Ser Ile Phe Leu Pro Tyr Leu Val Ser Leu Gly Gly
65
gtc aag agt ttg gat gaa tca ttg gtt cgt ggt gtt act ggt gat ttg
                                                                   288
Val Lys Ser Leu Asp Glu Ser Leu Val Arg Gly Val Thr Gly Asp Leu
cat agt ttt gtt tcc tca agt gcc tct gtc aat ggt tcc gtt tat ggt
                                                                   336
His Ser Phe Val Ser Ser Ser Ala Ser Val Asn Gly Ser Val Tyr Gly
            100
ttc cca caa tac ttg tgc tca aac ttt tta ttg tcc tca cca aat ggt
                                                                   384
Phe Pro Gln Tyr Leu Cys Ser Asn Phe Leu Leu Ser Ser Pro Asn Gly
                            120
act caa caa gca tct tcc ctt tta gaa ttg gct caa aag gtt ggt tat
                                                                   432
Thr Gln Gln Ala Ser Ser Leu Leu Glu Leu Ala Gln Lys Val Gly Tyr
    130
                        135
gaa caa att gtt tat cca gat gtt gcc tct tct agt tct ttc aca gtt
Glu Gln Ile Val Tyr Pro Asp Val Ala Ser Ser Ser Phe Thr Val
                    150
ttc gga ttg tat caa caa tta ctc caa tca tca tca gct gca gtt
                                                                   528
Phe Gly Leu Tyr Gln Gln Leu Leu Gln Ser Ser Ser Ala Ala Val
gat atc aag gcc tct gat ctt cca caa tct ggt gac caa gtc aac aag
Asp Ile Lys Ala Ser Asp Leu Pro Gln Ser Gly Asp Gln Val Asn Lys
```

gat ato					_			_	_			_		_	624
tct caa Ser Glr 210	Arg	_					_	_							672
aac tad Asn Tyr 225															720
atc aga Ile Arg															768
cca tad Pro Tyr															816
gaa aag Glu Lys		_	_	_	_	_	_		_			_			864
act tta Thr Leu 290	ı Val														912
aag aat Lys Asr 305															960
ttg ago Leu Sei				_	_	_	_	_	_	_	_	_	_	_	1008
tgt gtt Cys Val	_		_		_	_	_	_			_		_	_	1056
aga cca Arg Pro															1068
<210> 4 <211> 356 <212> PRT <213> Naegleria gruberi															
<400> 4 Met Sei 1		Gln	Pro 5	Lys	Thr	Leu	Thr	Val 10	Gly	Leu	Phe	Pro	Tyr 15	Leu	
Pro Sei	Trp	Asn 20	Glu	Asn	Gly	Asn	Glu 25	Val	Lys	Leu	Ile	Asn 30	Leu	Ile	

Lys Asp Val Leu Pro Thr Gln Val Ser Gly Tyr Asn Ile Glu Tyr Thr Glu Phe Asp Cys Tyr Ser Asp Ala Ser Leu Gln Ser Leu Pro Asp Val Phe Ser Thr Asp Ser Ile Phe Leu Pro Tyr Leu Val Ser Leu Gly Gly 75 Val Lys Ser Leu Asp Glu Ser Leu Val Arg Gly Val Thr Gly Asp Leu 85 His Ser Phe Val Ser Ser Ser Ala Ser Val Asn Gly Ser Val Tyr Gly Phe Pro Gln Tyr Leu Cys Ser Asn Phe Leu Leu Ser Ser Pro Asn Gly Thr Gln Gln Ala Ser Ser Leu Leu Glu Leu Ala Gln Lys Val Gly Tyr Glu Gln Ile Val Tyr Pro Asp Val Ala Ser Ser Ser Ser Phe Thr Val 150 155 Phe Gly Leu Tyr Gln Gln Leu Leu Gln Ser Ser Ser Ala Ala Val 170 Asp Ile Lys Ala Ser Asp Leu Pro Gln Ser Gly Asp Gln Val Asn Lys 180 185 Asp Ile Thr Gln Lys Tyr Arg Thr Ile Leu Asp Ser Thr Val Val Ala 200 Ser Gln Arg Glu Tyr Ile Asn Ser Val Lys Gln Gly Lys Pro Ile Ser 210 Asn Tyr Tyr Val Gly Tyr Ser Glu Ser Met Cys Glu Ile Lys Asp Ile Ile Arg Asp Gln Gln Tyr Asn Val Gln Leu Ile Gly Thr Ser Asp Lys Pro Tyr Val Tyr Thr Asp Val Leu Ala Leu Asn Ser Asn Leu Cys Asp Glu Lys Gln Lys Val Ala Val Glu Val Ile Lys Asn Leu Leu Thr Asn Thr Leu Val Leu Asp Leu Leu Gly Leu Gly Leu Thr Leu Pro Ala Asn Lys Asn Gly Ile Ala His Leu Ala Lys Ser Ser Asn Phe Tyr Ala Gln 315 Leu Ser Gln Gln Phe Asp Ala Lys Glu Ser Glu Val Arg Val Leu Arg

325

Cys Val Asp Phe Ala Asn Lys Glu Val Lys Asn Cys Ala Gly Val Leu 340 345 350

Arg Pro Phe Leu 355

<210> 5

<211> 412

<212> PRT

<213> Saccharomyces cerevisiae

<400> 5

Ala Asp Asp Val Lys Gln Leu Lys Ser Lys Phe Gly Phe Asn Pro Asp 1 5 10 15

Lys Ser Phe Val Val Pro Gln Glu Val Tyr Asp His Tyr Gln Lys Thr 20 25 30

Ile Leu Lys Pro Gly Val Glu Ala Asn Asn Lys Trp Asn Lys Leu Phe 35 40 45

Ser Glu Tyr Gln Lys Lys Phe Pro Glu Leu Gly Ala Glu Leu Ala Arg
50 . 55 60

Arg Leu Ser Gly Gln Leu Pro Ala Asn Trp Glu Ser Lys Leu Pro Thr 65 70 75 80

Tyr Thr Ala Lys Asp Ser Ala Val Ala Thr Arg Lys Leu Ser Glu Thr 85 90 95

Val Leu Glu Asp Val Tyr Asn Gln Leu Pro Glu Leu Ile Gly Gly Ser 100 105 110

Ala Asp Leu Thr Pro Ser Asn Leu Thr Arg Trp Lys Glu Ala Leu Asp 115 120 125

Phe Gln Pro Pro Ser Ser Gly Ser Gly Asn Tyr Ser Gly Arg Tyr Ile 130 135 140

Arg Tyr Gly Ile Arg Glu His Ala Met Gly Ala Ile Met Asn Gly Ile 145 150 155 160

Ser Ala Phe Gly Ala Asn Tyr Lys Pro Tyr Gly Gly Thr Phe Leu Asn 165 170 175

Phe Val Ser Tyr Ala Ala Gly Ala Val Arg Leu Ser Ala Leu Ser Gly
180 . 185 190

His Pro Val Ile Trp Val Ala Thr His Asp Ser Ile Gly Val Gly Glu
195 200 205

Asp Gly Pro Thr His Gln Pro Ile Glu Thr Leu Ala His Phe Arg Ser 210 225 220

Leu Pro Asn Ile Gln Val Trp Arg Pro Ala Asp Gly Asn Glu Val Ser 225 230 235 240

Ala Ala Tyr Lys Asn Ser Leu Glu Ser Lys His Thr Pro Ser Ile Ile
245 250 255

Ala Leu Ser Arg Gln Asn Leu Pro Gln Leu Glu Gly Ser Ser Ile Glu 260 265 270

Ser Ala Ser Lys Gly Gly Tyr Val Leu Gln Asp Val Ala Asn Pro Asp 275 280 285

Ile Ile Leu Val Ala Thr Gly Ser Glu Val Ser Leu Ser Val Glu Ala 290 295 300

Ala Lys Thr Leu Ala Ala Lys Asn Ile Lys Ala Arg Val Val Ser Leu 305 310 315 320

Pro Asp Phe Phe Thr Phe Asp Lys Gln Pro Leu Glu Tyr Arg Leu Ser 325 330 335

Val Leu Pro Asp Asn Val Pro Ile Met Ser Val Glu Val Leu Ala Thr 340 345 350

Thr Cys Trp Gly Lys Tyr Ala His Gln Ser Phe Gly Ile Asp Arg Phe 355 360 365

Gly Ala Ser Gly Lys Ala Pro Glu Val Phe Lys Phe Phe Gly Phe Thr 370 375 380

Pro Glu Gly Val Ala Glu Arg Ala Gln Lys Thr Ile Ala Phe Tyr Lys 385 390 395 400

Gly Asp Lys Leu Ile Ser Pro Leu Lys Lys Ala Phe
405
410

<210> 6

<211> 398

<212> PRT

<213> Craterostigma plantagineum

<400> 6

Pro Lys Glu Ala Glu Ala Thr Arg Lys Asn Leu Gly Trp Pro Tyr Glu

1 5 10 15

Pro Phe His Val Pro Asp Asp Val Lys Lys His Trp Ser Arg His Ile 20 25 30

Ala Glu Gly Ala Ala Leu Glu Ser Ala Trp Asn Ala Lys Phe Ala Glu
35 40 45

Phe Gln Lys Lys Phe Pro Glu Glu Ala Ala Asp Leu Lys Ser Ile Ile 50 55 60

Thr Gly Glu Leu Pro Thr Asn Trp Glu Ser Ile Phe Pro Thr Tyr Thr 65 70 75 80

Pro Glu Asn Pro Gly Leu Pro Thr Arg Thr Leu Ser His Gln Ile Leu 85 90 95

Asn Gly Leu Gly Asp Val Leu Pro Gly Leu Leu Gly Gly Ser Ala Asp 105 Leu Thr Leu Ser Asn Met Ala Phe Leu Lys Asn Ser Gly Asp Phe Gln Lys Lys Ser Pro Gly Glu Arg Asn Val Lys Phe Gly Ala Arg Glu His Ala Met Gly Ser Ile Cys Asn Gly Leu Ala Leu His Ser Pro Gly Leu Leu Pro Tyr Cys Ala Thr Tyr Phe Val Phe Thr Asp Tyr Met Arg Ala Ala Met Arg Ile Ser Ala Leu Ser Lys Ala Arg Val Leu Tyr Ile Met 185 190 Thr His Asp Ser Ile Gly Leu Gly Glu Asp Gly Pro Thr His Gln Pro 200 Val Glu His Leu Ala Ser Phe Arg Ala Met Pro Asn Ile Leu Thr Leu 210 215 Arg Pro Ala Asp Gly Asn Glu Thr Ala Gly Ala Tyr Arg Ala Ala Val Gln Asn Gly Glu Arg Pro Ser Ile Leu Val Leu Ala Arg Gln Lys Leu 245 Pro Gln Leu Pro Gly Thr Ser Ile Glu Gly Val Ser Lys Gly Gly Tyr Val Ile Ser Asp Asn Ser Arg Gly Gly Asn Ser Lys Pro Asp Val Ile Leu Ile Gly Thr Gly Ser Glu Leu Glu Ile Ala Ala Arg Ala Gly Asp Glu Leu Arg Lys Glu Gly Lys Lys Val Arg Val Val Ser Leu Val Cys 315 Trp Glu Leu Phe Ala Glu Gln Ser Glu Lys Tyr Arg Glu Thr Val Leu Pro Ser Gly Val Thr Ala Arg Val Ser Val Glu Ala Gly Ser Thr Phe 345 Gly Trp Glu Arg Phe Ile Gly Pro Lys Gly Lys Ala Val Gly Ile Asp Arg Phe Gly Ala Ser Ala Pro Ala Glu Arg Leu Phe Lys Glu Phe Gly Ile Thr Val Glu Ala Val Val Ala Ala Ala Lys Glu Ile Cys 385

<210> 7

<211> 402

<212> PRT

<213> Escherichia coli

<400> 7

Glu Glu Glu Val Ala Leu Ala Arg Gln Lys Leu Gly Trp His His Pro 1 5 15

Pro Phe Glu Ile Pro Lys Glu Ile Tyr His Ala Trp Asp Ala Arg Glu 20 25 30

Lys Gly Glu Lys Ala Gln Gln Ser Trp Asn Glu Lys Phe Ala Ala Tyr 35 40 45

Lys Lys Ala His Pro Gln Leu Ala Glu Glu Phe Thr Arg Arg Met Ser 50 55 60

Gly Gly Leu Pro Lys Asp Trp Glu Lys Thr Thr Gln Lys Tyr Ile Asn 65 70 75 80

Glu Leu Gln Ala Asn Pro Ala Lys Ile Ala Thr Arg Lys Ala Ser Gln 85 90 95

Asn Thr Leu Asn Ala Tyr Gly Pro Met Leu Pro Glu Leu Leu Gly Gly
100 105 110

Ser Ala Asp Leu Ala Pro Ser Asn Leu Thr Ile Trp Lys Gly Ser Val

Ser Leu Lys Glu Asp Pro Ala Gly Asn Tyr Ile His Tyr Gly Val Arg 130 135 140

Glu Phe Gly Met Thr Ala Ile Ala Asn Gly Ile Ala His His Gly Gly 145 150 155 160

Phe Val Pro Tyr Thr Ala Thr Phe Leu Met Phe Val Glu Tyr Ala Arg
165 170 175

Asn Ala Ala Arg Met Ala Ala Leu Met Lys Ala Arg Gln Ile Met Val 180 185 190

Tyr Thr His Asp Ser Ile Gly Leu Gly Glu Asp Gly Pro Thr His Gln
195 200 205

Ala Val Glu Gln Leu Ala Ser Leu Arg Leu Thr Pro Asn Phe Ser Thr 210 215 220

Trp Arg Pro Cys Asp Gln Val Glu Ala Ala Val Gly Trp Lys Leu Ala 225 230 235 240

Val Glu Arg His Asn Gly Pro Thr Ala Leu Ile Leu Ser Arg Gln Asn 245 250 255

Leu Ala Gln Val Glu Arg Thr Pro Asp Gln Val Lys Glu Ile Ala Arg 260 265 270 Gly Gly Tyr Val Leu Lys Asp Ser Gly Gly Lys Pro Asp Ile Ile Leu 275 280 285

Ile Ala Thr Gly Ser Glu Met Glu Ile Thr Leu Gln Ala Ala Glu Lys 290 295 300

Leu Ala Gly Glu Gly Arg Asn Val Arg Val Val Ser Leu Pro Ser Thr 305 310 315 320

Asp Ile Phe Asp Ala Gln Asp Glu Glu Tyr Arg Glu Ser Val Leu Pro 325 330 335

Ser Asn Val Ala Ala Arg Val Ala Val Glu Ala Gly Ile Ala Asp Tyr 340 345 350

Trp Tyr Lys Tyr Val Gly Leu Lys Gly Ala Ile Val Gly Met Thr Gly 355 360 365

Tyr Gly Glu Ser Ala Pro Ala Asp Lys Leu Phe Pro Phe Gly Phe 370 375 380

Thr Ala Glu Asn Ile Val Ala Lys Ala His Lys Val Leu Gly Val Lys 385 390 395 400

Gly Ala

<210> 8

<211> 400

<212> PRT

<213> Bacillus subtilis

<400> 8

Lys Glu Glu Ser Lys Leu Thr Lys Glu Ala Tyr Ala Trp Thr Tyr Glu 1 5 10

Glu Asp Phe Tyr Val Pro Ser Glu Val Tyr Glu His Phe Ala Val Ala

Val Lys Glu Ser Gly Glu Lys Lys Glu Gln Glu Trp Asn Ala Gln Phe 35 40 45

Ala Lys Tyr Lys Glu Val Tyr Pro Glu Leu Ala Glu Gln Leu Glu Leu 50 55 60

Ala Ile Lys Gly Glu Leu Pro Lys Asp Trp Asp Gln Glu Val Pro Val 65 70 75 80

Tyr Glu Lys Gly Ser Ser Leu Ala Ser Arg Ala Ser Ser Gly Glu Val
85 90 95

Leu Asn Gly Leu Ala Lys Lys Ile Pro Phe Phe Val Gly Gly Ser Ala 100 105 110

Asp Leu Ala Gly Ser Asn Lys Thr Thr Ile Lys Asn Ala Gly Asp Phe 115 120 125

Thr Ala Val Asp Tyr Ser Gly Lys Asn Phe Trp Phe Gly Val Arg Glu 130 135 140

Phe Ala Met Gly Ala Ala Leu Asn Gly Met Ala Leu His Gly Gly Leu 145 : 150 : 155 : 160

Arg Val Phe Gly Gly Thr Phe Phe Val Phe Ser Asp Tyr Leu Arg Pro 165 170 175

Ala Ile Arg Leu Ala Ala Leu Met Gly Leu Pro Val Thr Tyr Val Phe 180 185 190

Thr His Asp Ser Ile Ala Val Gly Glu Asp Gly Pro Thr His Glu Pro 195 200 205

Val Glu Gln Leu Ala Ser Leu Arg Ala Met Pro Asn Leu Ser Leu Ile 210 215 220

Arg Pro Ala Asp Gly Asn Glu Thr Ala Ala Ala Trp Lys Leu Ala Val 225 230 235 240

Gln Ser Thr Asp His Pro Thr Ala Leu Val Leu Thr Arg Gln Asn Leu 245 250 255

Pro Thr Ile Asp Gln Thr Ser Glu Glu Ala Leu Ala Gly Val Glu Lys
260 265 270

Gly Ala Tyr Val Val Ser Lys Ser Lys Asn Glu Thr Pro Asp Ala Leu 275 280 285

Leu Ile Ala Ser Gly Ser Glu Val Gly Leu Ala Ile Glu Ala Gln Ala 290 295 300

Glu Leu Ala Lys Glu Asn Ile Asp Val Ser Val Val Ser Met Pro Ser 305 310 315 320

Met Asp Arg Phe Glu Lys Gln Ser Asp Glu Tyr Lys Asn Glu Val Leu 325 330 335

Pro Ala Asp Val Lys Lys Arg Leu Ala Ile Glu Met Gly Ser Ser Phe 340 345 350

Gly Trp Gly Lys Tyr Thr Gly Leu Glu Gly Asp Val Leu Gly Ile Asp 355 360 365

Arg Phe Gly Ala Ser Ala Pro Gly Glu Thr Ile Ile Asn Glu Tyr Gly 370 375 380

Phe Ser Val Pro Asn Val Val Asn Arg Val Lys Ala Leu Ile Asn Lys 385 390 395 400

<210> 9

<211> 391

<212> PRT

<213> Mycoplasma genitalium

<400> 9

Glu Val Asp Phe Gln Leu Phe Glu Lys Arg Thr Asn Thr Asn Phe Asn 1 5 10 15

Phe Phe Asn Tyr Pro Asp Ser Ile Tyr His Trp Phe Lys Gln Thr Val 20 25 30

Ile Glu Arg Gln Lys Gln Ile Lys Glu Asp Tyr Asn Asn Leu Leu Ile 35 40 45

Ser Leu Lys Asp Lys Pro Leu Phe Lys Lys Phe Thr Asn Trp Ile Asp 50 55 60

Ser Asp Phe Gln Ala Leu Tyr Leu Asn Gln Leu Asp Glu Lys Lys Val 65 70 75 80

Ala Lys Lys Asp Ser Ala Thr Arg Asn Tyr Leu Lys Asp Phe Leu Asn 85 90 95

Gln Ile Asn Asn Pro Asn Ser Asn Leu Tyr Cys Leu Asn Ala Asp Val 100 105 110

Ser Arg Ser Cys Phe Ile Lys Ile Gly Asp Asp Asn Leu His Glu Asn 115 120 125

Pro Cys Ser Arg Asn Ile Gln Ile Gly Ile Arg Glu Phe Ala Met Ala 130 135 140

Thr Ile Met Asn Gly Met Ala Leu His Gly Gly Ile Lys Val Met Gly 145 150 155 160

Gly Thr Phe Leu Ala Phe Ala Asp Tyr Ser Lys Pro Ala Ile Arg Leu 165 170 . 175

Gly Ala Leu Met Asn Leu Pro Val Phe Tyr Val Tyr Thr His Asp Ser 180 185 190

Tyr Gln Val Gly Gly Asp Gly Pro Thr His Gln Pro Tyr Asp Gln Leu 195 200 205

Pro Met Leu Arg Ala Ile Glu Asn Val Cys Val Phe Arg Pro Cys Asp 210 215 220

Glu Lys Glu Thr Cys Ala Gly Phe Asn Tyr Gly Leu Leu Ser Gln Asp 225 230 235 240

Gln Thr Thr Val Leu Val Leu Thr Arg Gln Pro Leu Lys Ser Ile Asp 245 250 255

Asn Thr Asp Ser Leu Lys Thr Leu Lys Gly Gly Tyr Ile Leu Leu Asp 260 265 270

Arg Lys Gln Pro Asp Leu Ile Ile Ala Ala Ser Gly Ser Glu Val Gln 275 280 285

Leu Ala Ile Glu Phe Glu Lys Val Leu Thr Lys Gln Asn Val Lys Val 290 295 300

Arg Ile Leu Ser Val Pro Asn Ile Thr Leu Leu Leu Lys Gln Asp Glu 305 310 315 320

Lys Tyr Leu Lys Ser Leu Phe Asp Ala Asn Ser Ser Leu Ile Thr Ile 325 330 335

Glu Ala Ser Ser Ser Tyr Glu Trp Phe Cys Phe Lys Lys Tyr Val Lys 340 345 350

Asn His Ala His Leu Gly Ala Phe Ser Phe Gly Glu Ser Asp Asp Gly 355 360 365

Asp Lys Val Tyr Gln Gln Lys Gly Phe Asn Leu Glu Arg Leu Met Lys 370 375 380

Ile Phe Thr Ser Leu Arg Asn 385 390

<210> 10

<211> 316

<212> PRT

<213> Methanococcus jannaschii

<400> 10

Met Val Lys Leu Ser Gly Val Tyr Lys Gly Met Arg Lys Gly Tyr Gly
1 5 10 15

Glu Thr Leu Ile Glu Leu Gly Lys Lys Tyr Glu Asn Leu Val Val Leu 20 25 30

Asp Ala Asp Leu Ser Gly Ser Thr Gln Thr Ala Met Phe Ala Lys Glu 35 40 45

Phe Pro Glu Arg Phe Phe Asn Ala Gly Val Ala Glu Gln Asn Met Ile
50 60

Gly Met Ala Ala Gly Leu Ala Thr Thr Gly Lys Ile Val Phe Ala Ser 65 70 75 80

Ser Phe Ser Met Phe Ala Ser Gly Arg Ala Trp Glu Ile Ile Arg Asn 85 90 95

Leu Val Ala Tyr Pro Lys Leu Asn Val Lys Ile Val Ala Thr His Ala 100 105 110

Gly Ile Thr Val Gly Glu Asp Gly Ala Ser His Gln Met Cys Glu Asp 115 120 125

Ile Ala Ile Met Arg Ala Ile Pro Asn Met Val Val Ile Ala Pro Thr 130 135 140

Asp Tyr Tyr His Thr Lys Asn Val Ile Arg Thr Ile Ala Glu Tyr Lys 145 150 155 160

Gly Pro Val Tyr Val Arg Met Pro Arg Arg Asp Thr Glu Ile Ile Tyr 165 170 175 Glu Asn Glu Glu Glu Ala Thr Phe Glu Ile Gly Lys Gly Lys Ile Leu 180 185 190

Val Asp Gly Glu Asp Leu Thr Ile Ile Ala Thr Gly Glu Glu Val Pro 195 200 205

Glu Ala Leu Arg Ala Gly Glu Ile Leu Lys Glu Asn Gly Ile Ser Ala 210 215 220

Glu Ile Val Glu Met Ala Thr Ile Lys Pro Ile Asp Glu Glu Ile Ile 225 230 235 240

Lys Lys Ser Lys Asp Phe Val Val Thr Val Glu Asp His Ser Ile Ile 245 250 255

Gly Gly Leu Gly Gly Ala Val Ala Glu Val Ile Ala Ser Asn Gly Leu 260 265 270

Asn Lys Lys Leu Leu Arg Ile Gly Ile Asn Asp Val Phe Gly Arg Ser 275 280 285

Gly Lys Ala Asp Glu Leu Leu Lys Tyr Tyr Gly Leu Asp Gly Glu Ser 290 295 300

Ile Ala Lys Arg Ile Met Glu Glu Met Lys Lys Glu 305 310 315

<210> 11

<211> 409

<212> PRT

<213> Bacillus thiaminolyticus

<400> 11

Met Ser Lys Val Lys Gly Phe Ile Tyr Lys Pro Leu Met Val Met Leu 1 5 10 15

Ala Leu Leu Val Val Val Ser Pro Ala Gly Ala Gly Ala Ala His
20 25 . 30

Ser Asp Ala Ser Ser Asp Ile Thr Leu Lys Val Ala Ile Tyr Pro Tyr 35 40 45

Val Pro Asp Pro Ala Arg Phe Gln Ala Ala Val Leu Asp Gln Trp Gln 50 55 60

Arg Gln Glu Pro Gly Val Lys Leu Glu Phe Thr Asp Trp Asp Ser Tyr 65 70 75 80

Ser Ala Asp Pro Pro Asp Asp Leu Asp Val Phe Val Leu Asp Ser Ile 85 90 95

Phe Leu Ser His Phe Val Asp Ala Gly Tyr Leu Leu Pro Phe Gly Ser , 100 105 110

Gln Asp Ile Asp Gln Ala Glu Asp Val Leu Pro Phe Ala Leu Gln Gly
115 120 125

Ala Lys Arg Asn Gly Glu Val Tyr Gly Leu Pro Gln Ile Leu Cys Thr 130 135 140

Asn Leu Leu Phe Tyr Arg Lys Gly Asp Leu Lys Ile Gly Gln Val Asp 145 150 155 160

Asn Ile Tyr Glu Leu Tyr Lys Lys Ile Gly Thr Ser His Ser Glu Gln 165 170 175

Ile Pro Pro Pro Gln Asn Lys Gly Leu Leu Ile Asn Met Ala Gly Gly
180 185 190

Thr Thr Lys Ala Ser Met Tyr Leu Glu Ala Leu Ile Asp Val Thr Gly
195 200 205

Gln Tyr Thr Glu Tyr Asp Leu Leu Pro Pro Leu Asp Pro Leu Asn Asp 210 215 220

Lys Val Ile Arg Gly Leu Arg Leu Leu Ile Asn Met Ala Gly Glu Lys 225 230 235 240

Pro Ser Gln Tyr Val Pro Glu Asp Gly Asp Ala Tyr Val Arg Ala Ser 245 250 255

Trp Phe Ala Gln Gly Ser Gly Arg Ala Phe Ile Gly Tyr Ser Glu Ser 260 265 270

Met Met Arg Met Gly Asp Tyr Ala Glu Gln Val Arg Phe Lys Pro Ile 275 280 285

Ser Ser Ser Ala Gly Gln Asp Ile Pro Leu Phe Tyr Ser Asp Val Val 290 295 300

Ser Val Asn Ser Lys Thr Ala His Pro Glu Leu Ala Lys Lys Leu Ala 305 310 315 320

Asn Val Met Ala Ser Ala Asp Thr Val Glu Gln Ala Leu Arg Pro Gln 325 330 335

Ala Asp Gly Gln Tyr Pro Gln Tyr Leu Leu Pro Ala Arg His Gln Val 340 345 350

Tyr Glu Ala Leu Met Gln Asp Tyr Pro Ile Tyr Ser Glu Leu Ala Gln 355 360 365

Ile Val Asn Lys Pro Ser Asn Arg Val Phe Arg Leu Gly Pro Glu Val 370 375 380

Arg Thr Trp Leu Lys Asp Ala Lys Gln Val Leu Pro Glu Ala Leu Gly 385 390 395 400

Leu Thr Asp Val Ser Ser Leu Ala Ser

<210> 12

<211> 13

```
<212> PRT
<213> Naegleria gruberi
<400> 12
Ala Ser Asp Leu Pro Gln Ser Gly Asp Gln Val Asn Lys
<210> 13
<211> 12
<212> PRT
<213> Naegleria gruberi
<400> 13
Thr Ile Leu Asp Ser Thr Val Val Ala Ser Gln Arg
                   5
<210> 14
<211> 15
<212> PRT
<213> Naegleria gruberi
<400> 14
Ser Ser Asn Phe Tyr Ala Gln Leu Ser Gln Gln Phe Asp Ala Lys
<210> 15
<211> 16
<212> PRT
<213> Artificial Sequence
<223> Description of Artificial Sequence: Primer
<400> 15
Cys Ala Arg Trp Ser Ile Gly Gly His Gly Ala Tyr Cys Ala Arg Gly
  1
                   5
                                      10
<210> 16
<211> 17
<212> PRT
<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence: Primer
Thr Thr Ile Gly Cys Arg Thr Cys Arg Ala Ala Tyr Thr Gly Tyr Thr
                                      10
Gly
<210> 17
<211> 22
```

<212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Primer	
<400> 17 tgtcggatat agtgaaagta'tg	22
<210> 18	
<211> 22 <212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Primer	
<400> 18 aaccttttgc ttttcatcac ac	22
<210> 19	
<211> 31 <212> DNA	
<213> Artificial Sequence	
<223> Description of Artificial Sequence: Primer	
<400> 19 gagatataca tatgtccact caaccaaaga c	31
<210> 20 <211> 33	
<212> DNA <213> Artificial Sequence	
<220> <223> Description of Artificial Sequence: Primer	
<400> 20 tatggatcct taaaggaatg gtctcaagac acc	33
<210> 21	
<211> 27 <212> DNA <213> Artificial Sequence	
<220>	•
<223> Description of Artificial Sequence: Primer <400> 21	
caataaaaag tttgagctca agtattg	27

```
<210> 22
<211> 13
<212> PRT
<213> Naegleria gruberi

<400> 22
Val Tyr Gly Phe Pro Gln Tyr Leu Cys Ser Asn Phe Leu
1 5 10

<210> 23
<211> 6
<212> PRT
<213> Naegleria gruberi

<400> 23
Gly Tyr Ser Glu Ser Met
```